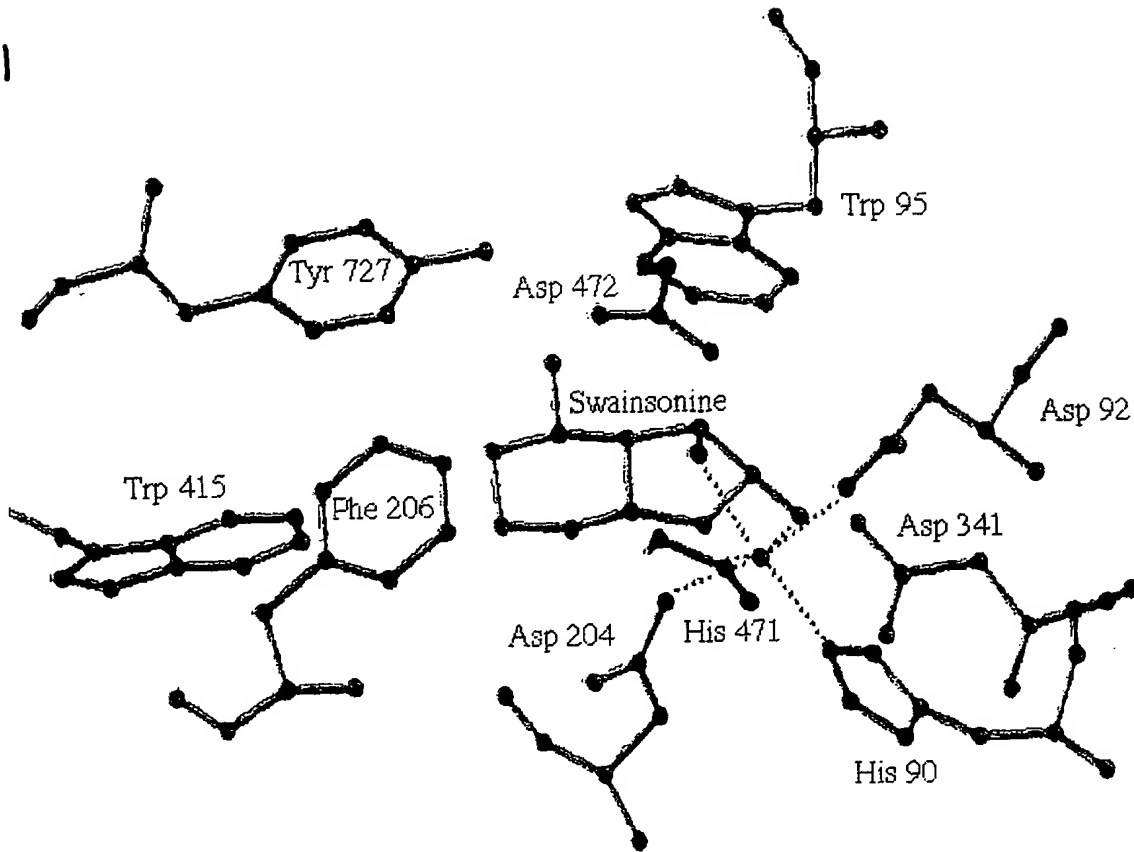


Fig. 1



**DATE** \_\_\_\_\_ **TIME** \_\_\_\_\_

Fig. 2



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Fig. 3

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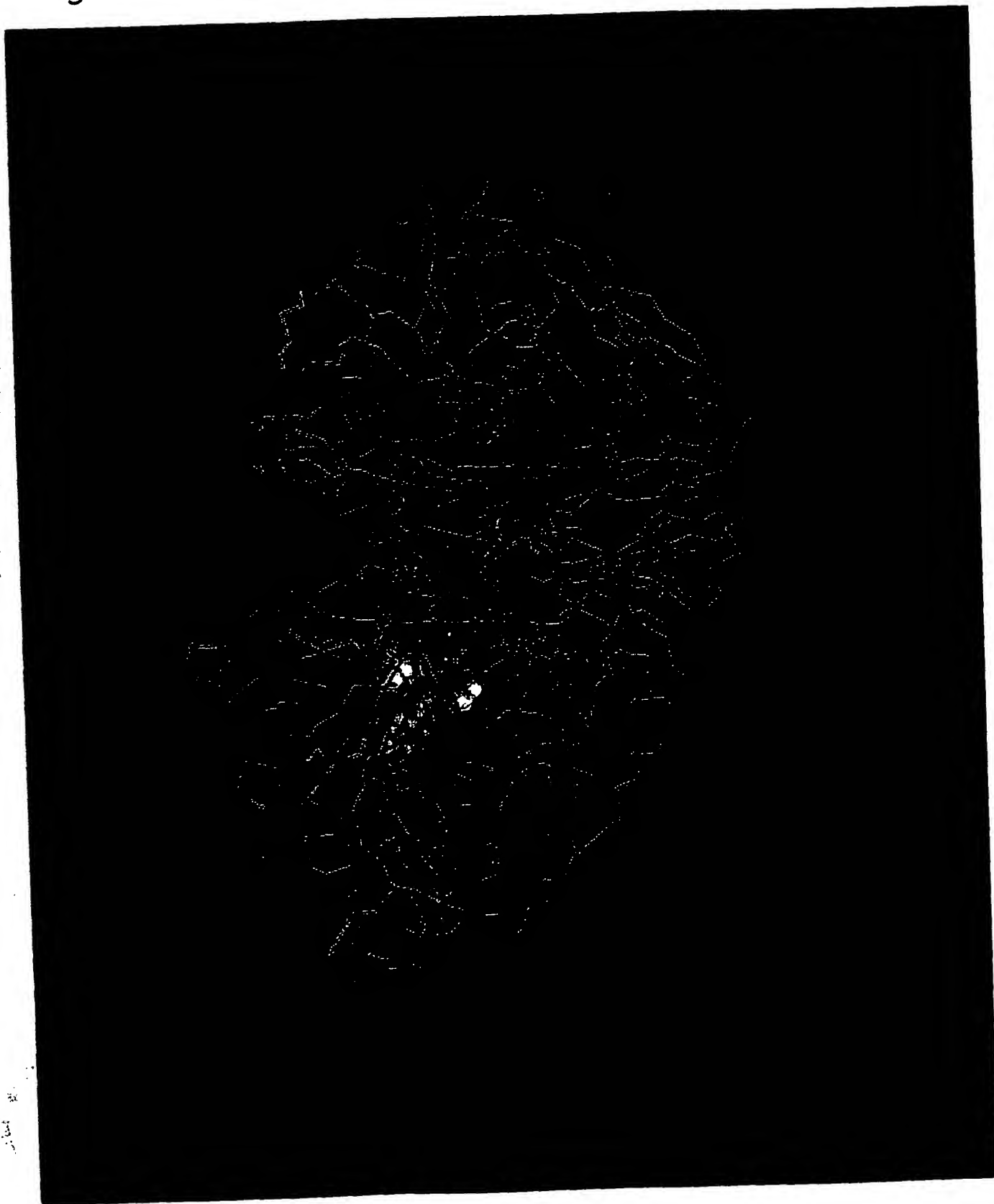
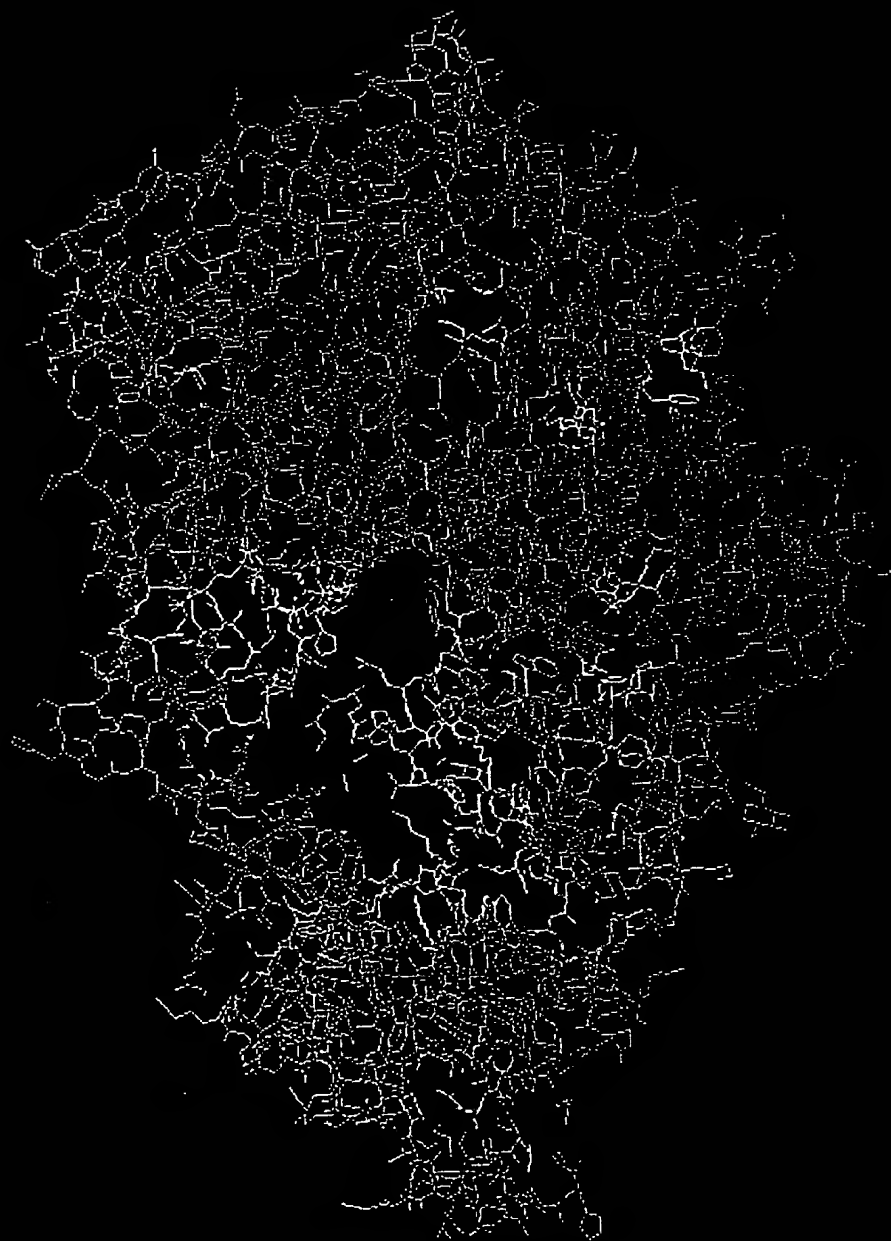
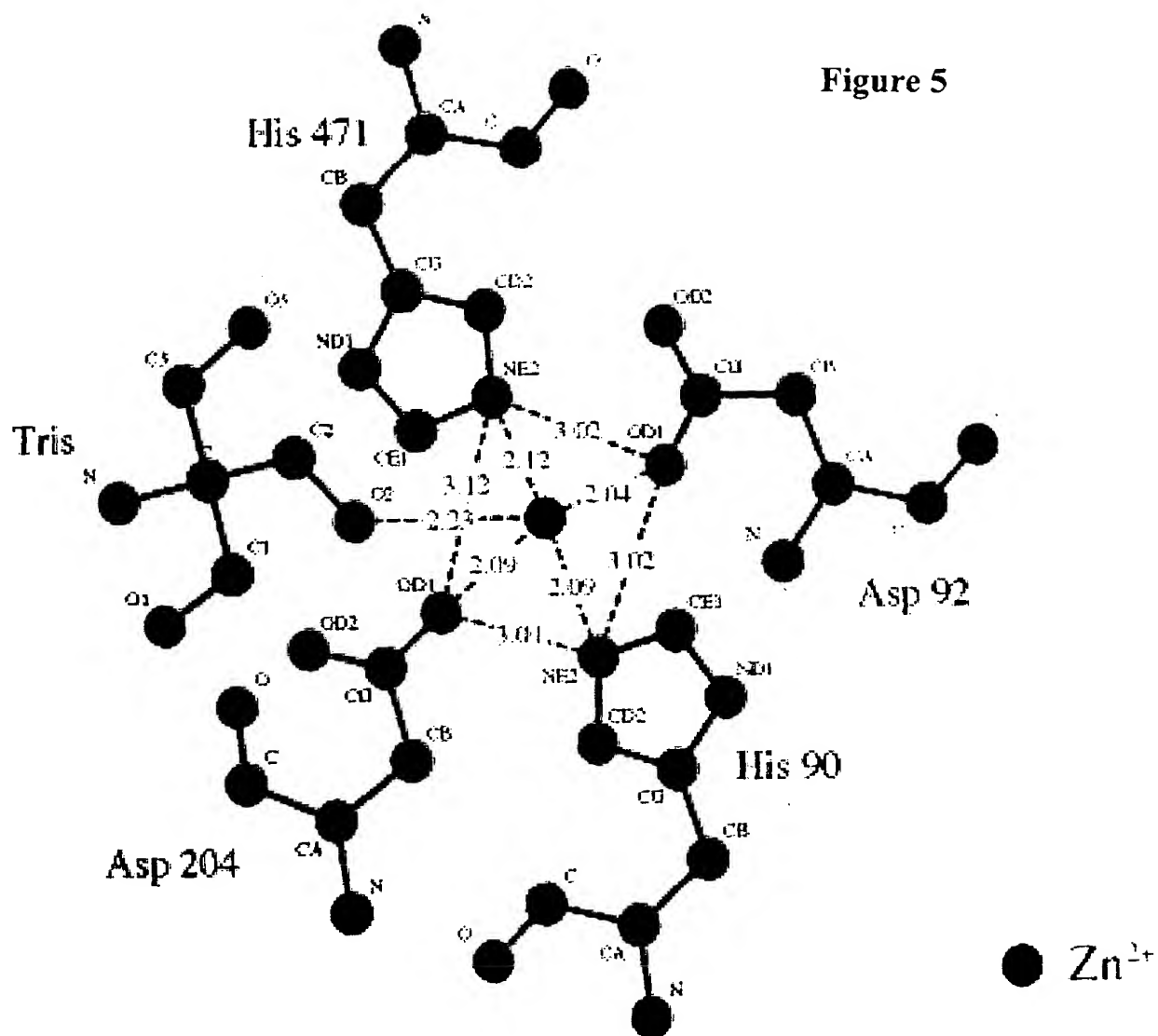


Fig. 4



205110-9220660

Figure 5



09960226.01502

pMT/BIP-N-HIS-dGMII [851 to 4042] -> 1-phase Translation

DNA sequence 6642 b.p. TCGCGGTTTCG ... AGGCCCTTTCGT circular

Figure 6

N-HIS added to pMTV5HisA (b/t BglIII/EcoRI) for drosophila expression of tagged proteins.  
Add drosophila dGMII from clone D11 (shortened 3') DAK/Tara 15-3-99

851/1 atg AAG TTA TGC ATA TTA CTG GCC GTC GTG 881/11 GCC TTT GTT GGC CTC TCG CTC GGG aga tct 911/21 agc cac cat cat cat cat cac gga gaa TTC  
H K L C I L L A V V A F V G L S L G R S S H H H H H H G E F  
941/31 gac gat cca ata aga cct cca ctt aaa gtg gct cgt tcc ccg agg cca ggg caa tgc caa gat gtg gtc caa gac gtg ccc aat gtg gat  
D D P I R P P L K V A R S P R P G Q C Q D V V V Q D V P N V D  
1031/61 gta cag atg ctg gag cta tac gat cgc atg tcc ttc aag gac ata gat gga ggc gtg tgg aaa cag ggc tgg aac att aag tac gat cca  
V Q M L E L Y D R M S F K D I D G G V W K Q G W N I K Y D P  
1121/91 ctg aag tac aac gcc cat cac aaa cta aaa gtc ttc gtt gtg ccg cac tgc aac aac gat cct gga tgg att cag acg ttt gag gaa tac  
L K Y N A H H K L K V F V V P H S H N D P G W I Q T F E E Y  
1211/121 tac cag cac gac acc aag cac atc ctg tcc aat gca cta cgg cat ctg cac gac aat ccc gag atg aag ttc atc tgg gcg gaa atc tcc  
Y Q H D T K H I L S N A L R H L H D N P E M K F I W A E I S  
1301/151 tac ttt gct cgt ttc tat cac gat ttg gga gag aac aaa aag ctg cag atg aag tcc att gta aag aat gga cag ttg gaa ttt gtg act  
Y F A R F Y H D L G E N K K L Q M K S I V K N G Q L E F V T  
1391/181 gga gga tgg gta atg ccg gac gag gcc aac tcc cac tgg cga aac gta ctg ctg cag ctg acc gaa ggg caa aca tgg ttg aag caa ttc  
G G W V M P D E A N S H W R N V L L Q L T E G Q T W L K Q F  
1481/211 atg aat gtc aca ccc act gct tcc tgg gcc atc gat ccc ttc gga cac agt ccc act atg ccg tac att ttg cag aag agt ggt ttc aag  
M N V T P T A S W A I D P F G H S P T M P Y I L Q K S G F K  
1571/241 aat atg ctt atc caa agg acg cac tat tgg gtt aag aag gaa ctg gcc caa cag cga cag ctt gag ttc ctg tgg cgc cag atc tgg gac  
M H L I Q R T H Y S V K K E L A Q Q R Q L E F L W R Q I W D  
1661/271 aac aaa ggg gac aca gct ctc ttc acc cac atg atg ccc ttc tac tgg tac gac att cct cat acc tgt ggt cca gat ccc aag gtt tgc  
N K G D T A L F T H M M P F Y S Y D I P H T C G P D P K V C  
1751/301 tgt cag ttc gat ttc aaa cga atg ggc tcc ttc ggt ttg agt tgt cca tgg aag gtg ccg ccg cgt aca atc agt gat caa aat gtg gca  
C Q F D F K R M G S F G L S C P W K V P P R T I S D Q N V A  
1841/331 gca cgc tca gat ctg ctg gtt gat cag tgg aag aag aag gcc gac ctg tat cgc aca aac gtg ctg ctg att ccg ttg ggt gac gac ttc  
A R S D L L V D Q W K K K A E L Y R T N V L L I P L G D D F  
1931/361 cgc ttc aag cag aac acc gag tgg gat gtg cag cgc gtg aac tac gaa agg ctg ttc gaa cac atc aac agc cag gcc cac ttc aat gtc  
R F K Q N T E W D V Q R V N Y E R L F E H I N S Q A H F N V  
2021/391 cag ggc cag ttc ggc aca ctg cag gaa tac ttt gat gca gtg cac cag ggc gaa agg ggc gca caa gcc gag ttt ccc acg cta agc ggt  
Q A Q F G T L Q E Y F D A V H Q A E R A G Q A E F P T L S G  
2111/421 gac ttt ttc aca tac gcc gat cga tog gat aac tat tgg agt ggc tac tac aca tcc cgc ccg tat cat aag cgc atg gac cgc gtc ctg  
D F F T Y A D R S D N Y W S G Y Y T S R P Y H K R M D R V L  
2201/451 atg cac tat gta cgt gca gca gaa atg ctt tcc gcc tgg cac tcc tgg gac ggt atg gcc cgc atc gag gaa cgt ctg gag cag gcc cgc  
M H Y V R A A E M L S A W H S W D G M A R I E E R L E Q A R  
2291/481 agg gag ctg tca ttg ttc cag cac cac gac ggt ata act ggc aca gca aaa acg cac gta gtc gtc gac tac gag caa cgc atg cag gaa  
R E L S L F Q H H D G I T G T A K T H V V V D Y E Q R M Q E  
2381/511 gct tta aaa gcc tgt caa atg gta atg caa cag tgc gtc tac cga ttg ctg aca aag ccc tcc atc tac agt ccg gac ttc agt ttc tgc  
A L K A C Q M V M Q Q S V Y R L L T K P S I Y S P D F S F S  
2471/541 tac ttt acg ctg gac gac tcc cgc tgg cca gga tct ggt gtg gag gac agt cga acc acc ata ata ctg ggc gag gat ata ctg ccc tcc  
Y F T L D D S R W P G S G V E D S R T T I I L G E D I L P S  
2561/571 aag cat gtg gtg atg cac aac acc ctg ccc cac tgg cgg gag cag ctg gtg gac ttt tat gta tcc agt ccg ttt gta agc gtt acc gac  
K H V V M H N T L P H W R E Q L V D F Y V S S P F V S V T D  
2651/601 ttg gca aac aat ccg gtg gag gct cag gtg tcc ccg gtg tgg agc tgg cac cac gac aca ctc aca aag act atc cac cca caa ggc tcc  
L A N N P V E A Q V S P V W S W H H D T L T K T I H P Q G S  
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T T K Y R I I F K A R V P P M G L A T Y V L T I S D S K P E  
2831/661 cac acc tgc tat gca tgc aat ctc ttg ctc cgt aaa aac ccg act tgc tta cca ttg ggc caa tat ccg gag gat gtg aag ttt ggc gat  
H T S Y A S N L L L R K N P T S L P L G Q Y P E D V K F G D  
2921/691 cct cga gag atc tca ttg cgg gtt ggt aac gga ccc acc ttg gcc ttt tgc gag cag ggt ctc ctt aag tcc att cag ctt act cag gat  
P R E I S L R V G N G P T L A F S E Q G L L K S I Q L T Q D  
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S P H V P V H F K F L K Y G V R S H G D R S G A Y L F L P N  
3101/751 gga cca gct tgc cca gtc gag ctt ggc cag cca gtc gtc ctg gtg act aag ggc aaa ctg gag tgc tcc gtg agc gtg gga ctt ccg agc  
G P A S P V E L G Q P V V L V T K G K L E S S V S V G L P S  
3191/781 gtg gtg cag cag atg ata atg cgc ggt ggt gca cct gag att cgc aat ctg gtg gat ata ggc tca ctg gac aac acg gag atc gtg atg  
V V H Q T I M R G G A P E I R N L V D I G S L D N T E I V M  
3281/811 cgc ttg gag acg cat atc gac agc ggc GAT ATC ttc tac acg gat ctc aat gga ttg caa ttt atc aag agg cgg cgt ttg gac aaa tta  
R L E T H I D S G D I F Y T D L N G L Q F I K R R R L D K L

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P L Q G N Y Y P I P S G M F I E G D A N C R L T L T L T T G G Q P L	P L Q G N Y Y P I P S G M F I E G D A N C R L T L T L T T G G Q P L	P L Q G N Y Y P I P S G M F I E G D A N C R L T L T L T T G G Q P L
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G G S S L A S G E L E I M Q D R R L A S D G D E R G L G Q G V	G G S S L A S G E L E I M Q D R R L A S D G D E R G L G Q G V	G G S S L A S G E L E I M Q D R R L A S D G D E R G L G Q G V
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L D N K P V L H I Y R L V L E K V N N C V R P S K L H P A G	L D N K P V L H I Y R L V L E K V N N C V R P S K L H P A G	L D N K P V L H I Y R L V L E K V N N C V R P S K L H P A G
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Y L T S A A H K A S Q S L L D P L D K F I F A E N E W I G A	Y L T S A A H K A S Q S L L D P L D K F I F A E N E W I G A	Y L T S A A H K A S Q S L L D P L D K F I F A E N E W I G A
3731/961	3761/971	3791/981
cag ggg caa ttt ggt ggc gat cat cct tcy gct cgt gag gat ctc gat gtg tcy gtg atg aga cgc tta acc aag agc tcy gcc aaa acc	cag ggg caa ttt ggt ggc gat cat cct tcy gct cgt gag gat ctc gat gtg tcy gtg atg aga cgc tta acc aag agc tcy gcc aaa acc	cag ggg caa ttt ggt ggc gat cat cct tcy gct cgt gag gat ctc gat gtg tcy gtg atg aga cgc tta acc aag agc tcy gcc aaa acc
Q G Q F G G D H P S A R E D L D V S V M R R L T K S S A K T	Q G Q F G G D H P S A R E D L D V S V M R R L T K S S A K T	Q G Q F G G D H P S A R E D L D V S V M R R L T K S S A K T
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cag cga gta ggc tac gtt ctg cac cgc acc aat ctg atg caa tgc ggc act cca gag gag cat aca cag aag ctg gat gtg tgc cac cta	cag cga gta ggc tac gtt ctg cac cgc acc aat ctg atg caa tgc ggc act cca gag gag cat aca cag aag ctg gat gtg tgc cac cta	cag cga gta ggc tac gtt ctg cac cgc acc aat ctg atg caa tgc ggc act cca gag gag cat aca cag aag ctg gat gtg tgc cac cta
Q R V G Y V L H R T N L H Q C G T P E E H T Q K L D V C H L	Q R V G Y V L H R T N L H Q C G T P E E H T Q K L D V C H L	Q R V G Y V L H R T N L H Q C G T P E E H T Q K L D V C H L
3911/1021	3941/1031	3971/1041
ctg ccg aat gtg gcy aga tgc gag cgc acg acg ctg act ttc ctg cag aat ttg gag cac ttg gat ggc atg gtg gcy ccg gaa gtg tgc	ctg ccg aat gtg gcy aga tgc gag cgc acg acg ctg act ttc ctg cag aat ttg gag cac ttg gat ggc atg gtg gcy ccg gaa gtg tgc	ctg ccg aat gtg gcy aga tgc gag cgc acg acg ctg act ttc ctg cag aat ttg gag cac ttg gat ggc atg gtg gcy ccg gaa gtg tgc
L P N V A R C E R T T L T F L Q N L E H L D G M V A P E V C	L P N V A R C E R T T L T F L Q N L E H L D G M V A P E V C	L P N V A R C E R T T L T F L Q N L E H L D G M V A P E V C
4001/1051	4031/1061	
ccc atg gaa acc gcc gct tat gtg agc agt cac tca agc TGA	ccc atg gaa acc gcc gct tat gtg agc agt cac tca agc TGA	
P M E T A A Y V S S H S S *	P M E T A A Y V S S H S S *	

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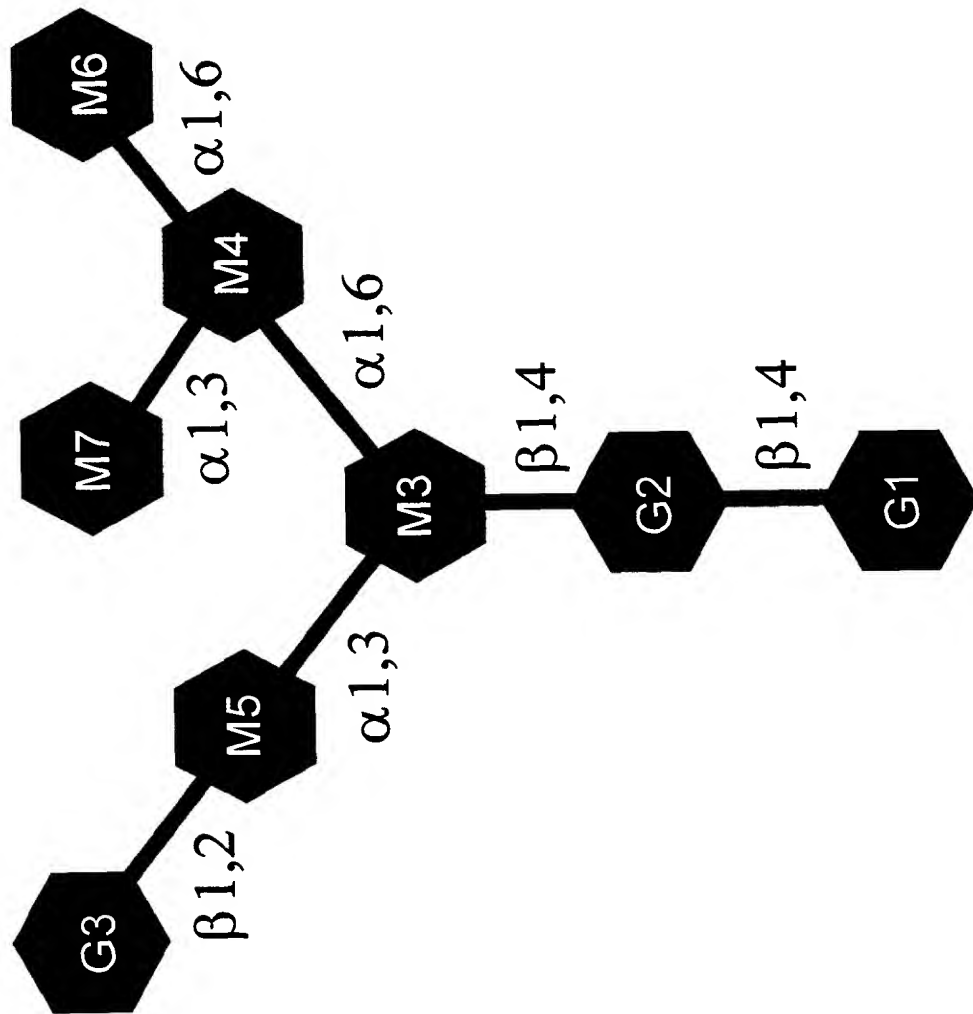
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| | | | |  
831 HGRIVSEVCPDYNVAVNUVLHQISQSVSNVUOVVYVRELA 880  
| | | | |  
793 RLETHDSGSDITFDLOLQVOTKEBELQVLOQVPIPSOWIEDANT 842  
| | | | |  
801 KISGDSQSGVPIVUQVLOQVOTKEBELQVLOQVPIPSOWIEDANT 930  
| | | | |  
843 RUTLQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 892  
| | | | |  
931 RUTLQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 980  
| | | | |  
893 RUTLEVAVNVVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 938  
| | | | |  
981 RULLEVAVNVVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 1077  
| | | | |  
939 VTCQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 986  
| | | | |  
1028 TLEQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 1076  
| | | | |  
987 C.....QVPS.....RUTVQVQVQVQVQVQVQVQVQVQVQV 1026  
| | | | |  
1077 CAPVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 1126  
| | | | |  
1027 VAPVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 1045  
| | | | |  
1127 VAPVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 1144

1027 VAPEVCPMEIAAYVSSH\$ 1045  
 . . . . .  
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2127 SEINLSPMEISTFRIGLR. 1144

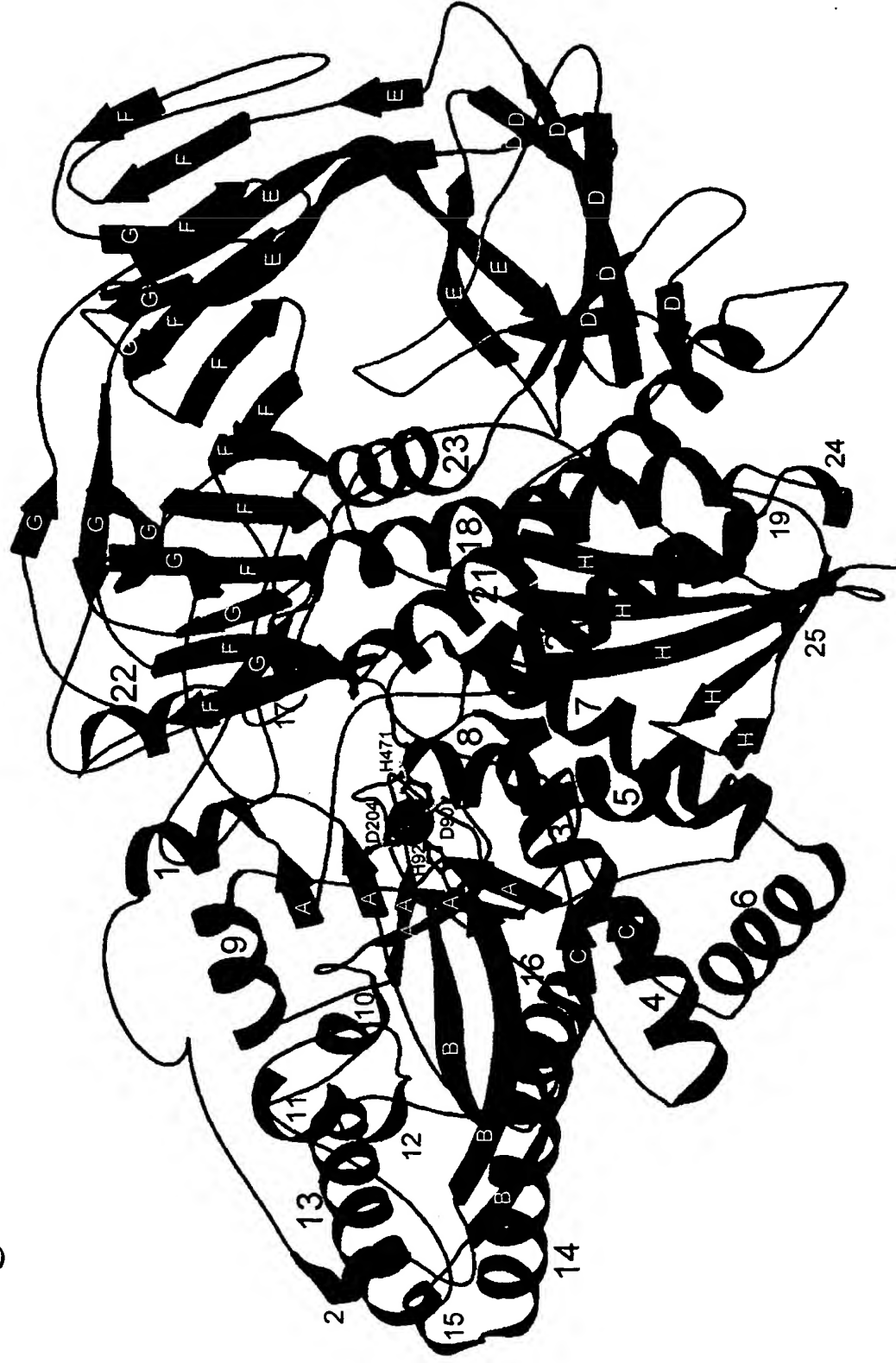


Figure 8A



205110-92209660

Figure 8B



205410-9620960

Figure 8C



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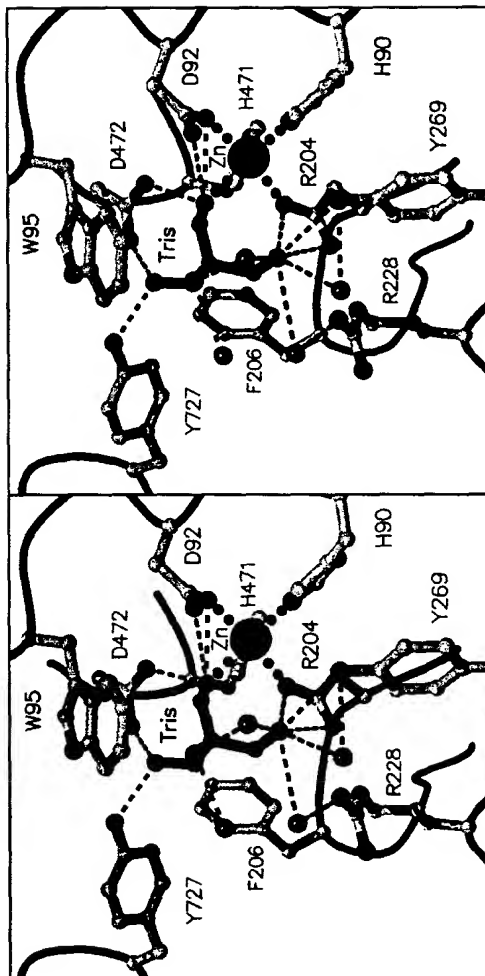




Figure 13



Figure 10A



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Figure 10B

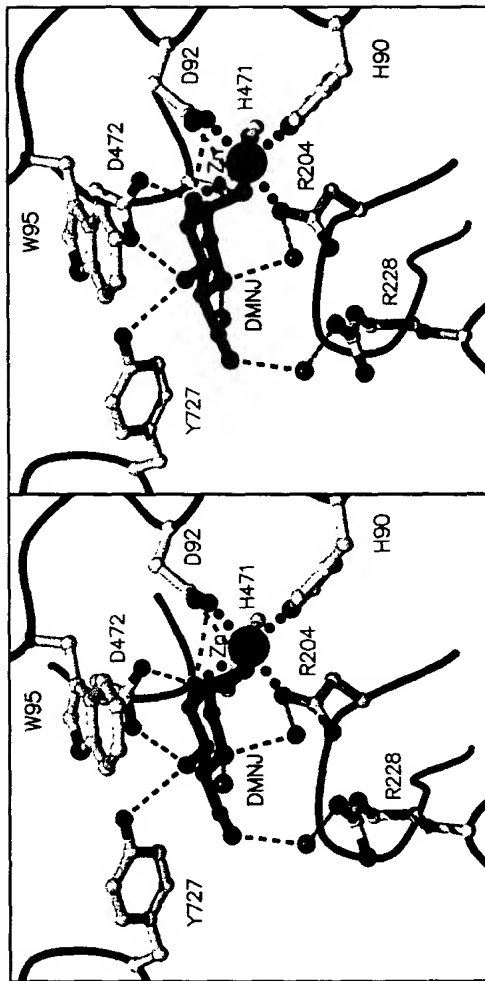




Figure 10C

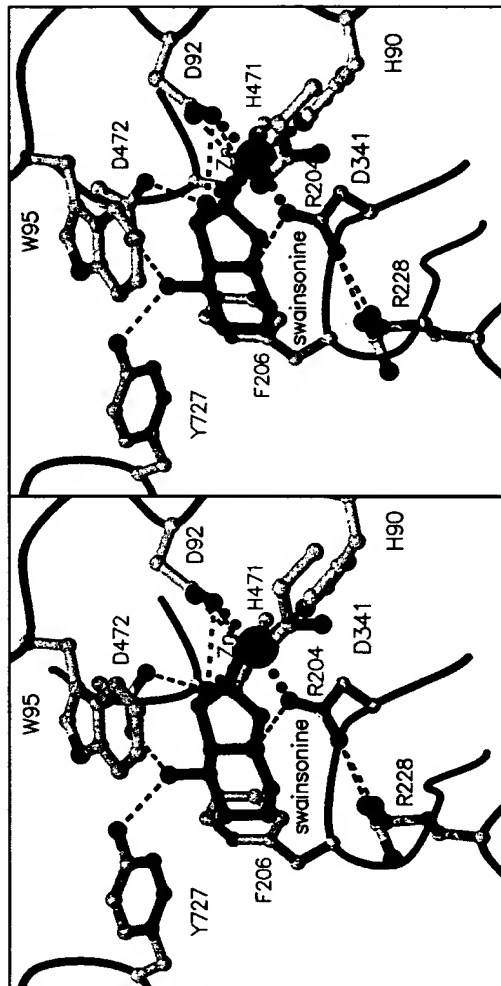
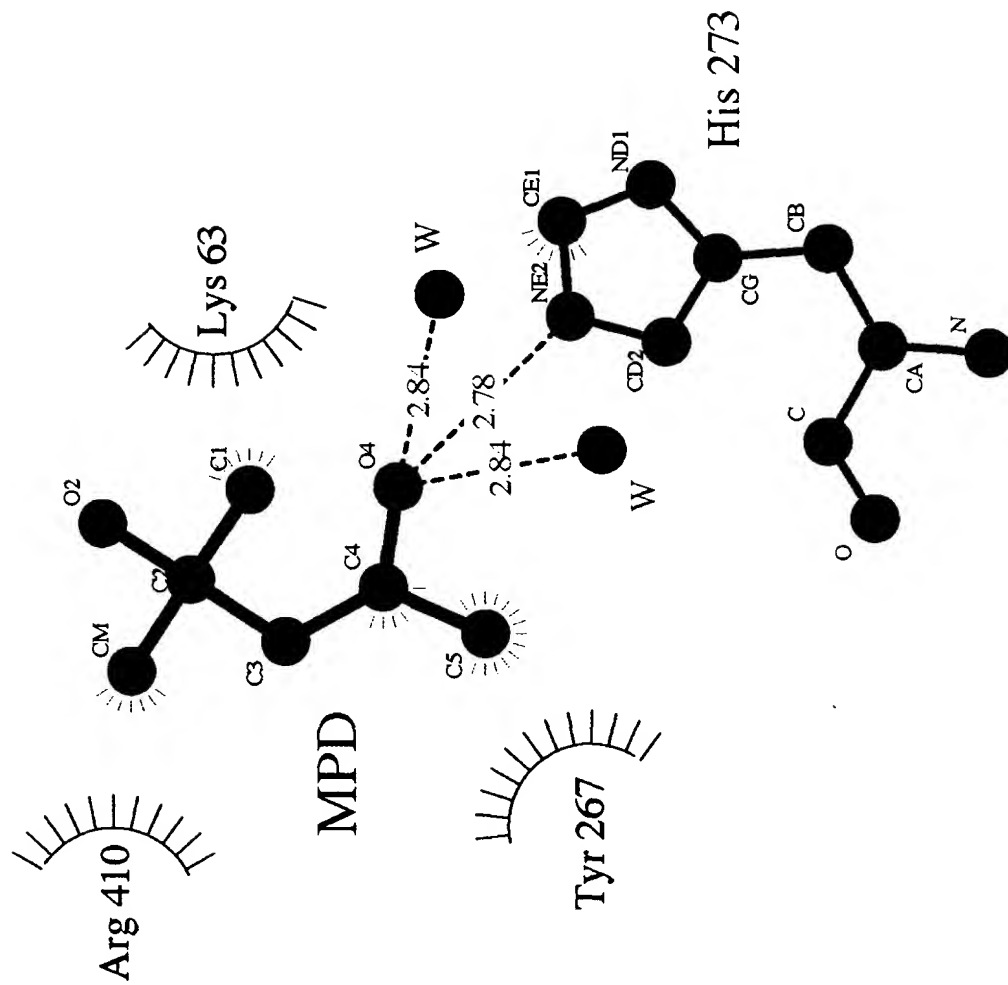


Figure 11A





Chemical structure diagram of a complex molecule, likely a mannosidase structure, showing a central core with multiple branching points and various functional groups.

09960226-011502

Figure 11C



20510-9209660